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	20		25		30										
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
	35		40		45										
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
	50		55		60										
Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
	65		70		75										80
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
			85					90						95	
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Ala
1			5			10			15						
Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala
			20			25			30						
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
		35			40				45						
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
		50			55				60						
Val	Ser	Ala	Gln	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu	
		65			70				75					80	
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
			85					90						95	
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Gln Thr Val Glu Asp Gln Ala Arg Arg Met Trp Ala Ser Ala

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp	Glu	Ala	Arg	Arg	Met	Trp	Ala	Ser	Ala	Gln	Asn	Ile	Ser	Gly
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Trp	Ala	Ser	Ala	Gln	Asn	Ile	Ser	Gly	Ala	Gly	Trp	Ser	Gly
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln	Asn	Ile	Ser	Gly	Ala	Gly	Trp	Ser	Gly	Met	Ala	Glu	Ala	Thr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Gly	Trp	Ser	Gly	Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln	Gln	Gln	Gln	Ala	Ser
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ala	Ser	Arg	Phe	Met	Thr	Asp	Pro	His	Ala	Met	Arg	Asp	Met	Ala
1				5				10						15	
Gly															

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln
1			5					10					15		

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids

58

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15
Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

59

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

60

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Gly Leu Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Ser	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala	Glu	His	Gln	Ala	Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1			5				10					15		

(3) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1			5				10					15		

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala	Ala	Cys	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Thr	Thr	Asn	Phe	Phe	Gly	Val	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Asn
1			5					10					15		
Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile							
			20				25								

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn	Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile	Gln	Ala	Ala	Thr	Val	Met
1			5					10					15		
Ser	His	Tyr	Gln	Ala	Val	Ala	His	Glu							
			20				25								

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

TSAGCGCCAA CCTACCGTC GGTTCCTCAC ACCGACCGCA TGGCTTGCTC CGCGGACTGC      60
CGCTAGGGTC GCGGATCACT CCGCGTAGCG GCGCCTTTTC CCACCGATAT GGGTTCCGTC      120
ACAGTGTGGT TGCCCGCCCG CCATCGGCCG GATAACGCCA TGAUCTCAGC TCGGCAGAAA      180
TGACAATGCT CCAACAGCG TGAGCACTCG AAGACAACCTA AGCAGGAGAT CGCATGCCGT      240
TTGTGACTAC CCAACCAGAA GCACTGCGCG CCGCGGCCCG CAGTCTGCAG GGAATCGGCT      300
CCGCATTGAA CGCCCGAAT GCGCTGCGG CCACTCCAC GACGGGGTG GTCCGGGGC      360
CGCCGATGAA NTGTGCGCG TGACGGCGCG TCAGTTGCG GCACACGCC AGATCTATCA      420
GGCCTTCAGC GCGCAGCGG CCGCGATTCA CGAGATGTTT GTCAACACTC TACAGATGAG      480
CTCAGGGTCC TATGCTGCTA CCGAGGCCCG CAACCGCGCC GCGGCGGNT AGAGGAGTCA      540
CTGCGATGGA TTGCGGCGG TTGCGGCCG AGGTCAATTG GGTGCGGATG TATGCCGTTT      600
CTGCTCGGC ACCAATGCT GCTGCGGCT CCGCTGGAA CGGTTGGCC GCGGAGCTGA      660
GTTGCGCGCG CACCGGTTAT GAGACGTTGA TCACTCAGCT CAGCACTGAG GGGTGGCTAG      720
GTCCCGCGTC AGCGCGATG GCGAGGCAG TTGCGCGTA TGTGGCGTGG ATGAGTGGG      780
CTGCGCGGCA AGCGAGCAG GCGGCCACAC AGGCCAGGCC CCGCGCGGCC GCTTTTGAGG      840
CGCGGTTTGC CCGAGCGTG CCGCGCGGT TGATCGCGG CAACCGGCT TCGTTGATGC      900
AGCTGATCTC GACGAATTC TTGCTCAGA ACACCTCGG GATCGCGGCC GCGGAACCTC      960
AGTACGG

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala
1           5           10          15

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala Asn Leu Gln Gly
1           5           10          15

```

(2) INFORMATION FOR SEQ ID NO:86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu Ala Ala Ala Ala Asn Leu Gln Gly Ile Gly Thr Thr Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:88:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala Ala Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:89:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Gln Asn Ala Ala Ala Ala Pro Thr Thr Gly Val Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu	Val	Ser	Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe
1				5				10							15

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
1			5						10					15

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly
1			5						10					15

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr
1			5						10					15

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

ATTGCTTCCT GCGCAGCTA AATCCCGGGG ACATCGTCCG CCGCCAGTAC GAGGTCAAAG      60
GCTGCAATCC GCACGGGCGA CTGGGCTGGA TCTACCTCCG TCTCGACCCG AATGTCAAAG      120
GCCGTCCGGT GGTGCTCAAG GGCTTGTTC ATTCCGGTGA TCCCGAAGCG CAGGCAATCG      180
CGATGCGCGA ACCCCAGTTC CTGGCCGAGG TGGTGCACCC GTCGATCGTG CAGATCTTCA      240
ACTTTGTGCA GCACACCGAC AGGCACGGGG ATCCGGTCCG CTACATCGTG ATGGATACG      300
TCGGCGGGCA ATCGCTCAAA CCGACCAAGG GTCANAACT GCCCTCCCG GAGGCCATCG      360
CCTACCTGCT GGAGATCTTG CCGCGCTGA GCTACCTGCA TTCCATCGGC TTGCTCTACA      420
ACGACCTGAA GCGGGAAGAC ATCATGCTGA CCHAGGAACA GCTCAAGCTG ATCGACCTGG      480
GCGCGGTATC GCGGATCAAC TCGTTGGGCT ACCCTCTACG GACCCGAGGC TTCCAGGCGC      540
CCGAGATCGT GCGGACCGGT CCGACGGTGG CCACCGACAT CTACACCGTG GGACCGACCG      600
TCGCGGGGCT CACGCTGGAC CTGCCCCACC GCAATGGCCG TTATGTGGAT GGGCTACCCG      660
AAGACGACCC GGTGCTGAAA ACCTACGACT CTTCGGGCGG GTTGCTGCGC AGGGCCATCG      720
ACCTCGATCC GCGGCAACCG TTCAACACCG CCGAAGAGAT GTCCGCGCAA TTGACGGGCG      780
TGTTCGCGGA GGTGCTGCGC CAGACACCGG GGTGCGGCGG CCAGGCTATC AACGATCTTC      840
AGTCCCAATC GGTGACATTT TGGAGTGGAC TGCTGCTGGC GCACACCGAC GTGTATCTGG      900
ACGGGCAGGT GCACGCGGAG AAGCTGACCG CCAACGAGAT CCGACCGCGG CTGTGCGTGC      960
CGCTGCTGCA TCGACCGGAC GTGCGAGCTT CGGTCTTCCA GCGCACGGTG CTCTCCAGC      1020
CGGTGCAGAC CCTAGACTCG GTGCGCGCGG CCGCGCACCG TCGGCTGGAC GTCGACGGCG      1080
TCGATINTCC GAGTCAGTGG AGCTGCGGCT AATGGAAGTC CCGCGGCTGC TGGATCTCGG      1140
CGATGTGGCC AAGGCCACCC GAAAACTCGA CGATCTGGCC GAACGCGTTC GTGCGCGATG      1200
GCGATTGGTC TGATACCGGG CCGTCCCGGA GCTGCTCACC GCGGACTATG ACTCGGCCAC      1260
CAACATTTTC ACCGAGGTGC TGGATACCTT TCGGCGCGAG CTGGCGGCTT AGCTCGGCCCT      1320
GGCCGCGTCC GCGGAACGAC CCGGCAACAC CGACGAACAC AAGTTCTATC AGACGGTGTG      1380
GAGCACCACG GACGGCGTGA TCTCGGCGGC TTTEGGACTG GCGAGAGCCC GGTCCGCGCA      1440
AGGTGATCGG GTCGGCGCGG TCGGACGCTT CGACGAGCTA CCGCCACTT CTCGGCATTT      1500

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CACCACGGCA	CGGCTGACCA	GGCGGGTGAC	TCTGTTTCTC	GGCGGTCGA	CGAGTGAAGT	1560
CACCGAGGAA	CAGATCCGCG	ACGCCCCCTG	AAGAGTGGAG	GGGCTGCCCC	CGACCGAATC	1620
ACGCGTSCCTG	CAGATCCGCG	CCCTGGTGCT	GGGTGGCGCG	CTGGACTGGC	TGAAGGACAA	1680
CAAGGCCAGC	ACCAACCACA	TCTCGGTTT	CCCGTTCACC	AGTCACGGGT	TGCGGCTGGG	1740
TGTGAGGCG	TCACTGGGCA	GGTGGCCCCG	GGTAGCTCCC	ACTC		1784

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACAARACACT	CGGCGCGCG	CGGTCCGGCC	TGATCGTGGG	TGATCAGCTT	CGTGCCAAAY	60
TGGGCACAAAG	GTGCGCGCTT	CCCAAGAGCT	TCTTCGCGCG	GTTCGCGGCM	KAACCTGCGCT	120
ATCCTGGTTG	GGTGGCGTCC	CCCAAAACCC	GGGAACPTAA	ACCCATTTTA	ACCGGSCAGG	180
AAGTTTCTTA	CATYIACCCN	GGSMANCCAA	CGGGGCGCGC	NANAAMTCCG	TCCTGGANTC	240
CGANCGGTTT	CGGTGTTCG	CCGCACTGCT	GACCGGCACG	GARTATCCGC	AGCGGCGGTT	300
GGCCAAACCG	TGGGTGCAAC	TGGCCTACGG	TGCGCACCCG	GACGCCATCA	CCGCTCGGA	360
GTCCGACCCAG	GTACTCAATG	CTGGCGACCA	CACCGGCCAG	CGACCCAAAC	TGGTGCCACGC	420
CGATCTCCAG	GGCGCGCGCG	CCGGTGGCAT	ACGGATTGGT	CGAAACCAAT	CCGAAGGAAT	480
TCATCACCGA	CGGTACCGGA	AAACGATCCG	CCCAATGGGN	GGACNACCCN	AGCCAGGCCG	540
ATTACCGGTT	NAACAAAGTT	GGTAGGTTT	TTTGATATCG	AKCAACCGAT	ACCGAGCGGM	600
CGCGGAATG	GTAGACCACC	ACCACTGCCC	NCAMGTMTG	CACCAAGTTT	GTTCATCGCCC	660
GCAGATCGGT	GACCGCGGCA	AGCGTTCCGG	ATGCGGAGAT	GAGGTTGACC	AGCCYGGTTG	720
ACCTGTTGAT	CAGGTTTCTC	CAGTGGCAGG	TGGSCAGCTG	GCCGCT		766

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGGCACBAGA	ATGTGCGCTG	TGCCTCGATA	GCCACTTGCG	TGTGGTCCCG	CTGCCAGCGG	60
GTACGCCAGG	TGGCTGCTC	CAGGCCATCG	GGCGGCGCGA	GGAGCGCGAT	GTTGGCCAGA	120
CCGCTGTGAC	GAGAACCGGA	CTCGACNAAG	TGTGCGCGCT	GACGCGCGCT	CAGTTCCCGG	180
CACACGCCCA	GATCTATCAG	GCGCTCAGCG	CCGAGGCCCG	GGCGATTCA	GAGATGTTCC	240
TCAACACTCT	ACAGATNANC	TCAGGGTCGT	ATGCTGCTAC	CGAGGCGGCC	AACGCGGCCG	300
CGGCGGCTA	GAGGAGTCAC	TCCGATGGAT	TTTGGGCGCT	TECCGCGCGA	GGTCAATTCG	360
GTGCGGATGT	ATGCGGCTTC	TGGCTCGGCA	CCAATGCTCG	CTGCGGCGTC	GGCCTGGAAC	420
GGGTTGGCCG	CGAGCTGAG	TTGCGCGGCC	ACCGGTTATG	AGACGCTGAT	CACTCAGCTC	480
AGCAGTGAGG	GCTGGCTAGG	TCCGCGCTCA	GCGCGGATGG	CCGAGGCACT	TGCGCGGTAT	540
GTGCGGTTGA	TGAGTGCGCG	TGCGCGCGCA	GCTGAGCAGG	CGGCCACACA	GGCCAGGCGC	600
GCGCGGCGCG	CTTTTGAGGC	GCGGTTTGCT	GCGAGCGCTC	CTCGCGCGCT	GATCGCGGCC	660

AACCGGGCTT	CGTTGATGCA	GCTGATCTCG	ACGAATGTCT	TTGCTCAGAA	CACCTCGGCG	720
ATCGCGGCC	CGAAGCTCA	GTACGGCGAG	ATGTGGGCC	AAGACTCCGC	GGCAATGTAT	780
GCTACGCGG	GCAGTTCCGC	GAGCGCCTCG	GCGGTCAAGC	CGTTTAGCAC	GGCGCGCCAG	840
ATTGCCAACC	CGACCCCTCA	GGGTACGCG	GCCGCGGCCG	TGGCCACCGC	CGCGGTACC	900
GCCCACTCGA	CGCTGACGGA	GATGATCAAC	GGGCTACCCA	ACGCGCTGCA	AAGCCTCACC	960
TCACTCTGT	TCCAGTCCTC	TAACGGTCCG	CTGCTCTGGC	TGTGGCAGAT	CTGTTCGGGC	1020
ACGCCCCATT	TCCCCACCTC	AATTTCCGCA	CTGCTGACCG	ACCTGCAGCC	CTACCGGAGC	1080
TTTNTTATA	ACACCGAGGG	CTTCCCTAC	TTGAGCATCG	GCATGGGCAA	CAACTTCATT	1140
CAGTCGGCCA	AGACCTCTGG	ATTGATCGGC	TAGGCGGCAC	CGGCTGCGGT	CGCGCTGCT	1200
GGGATNCCG	CCAGGGGCTT	GCCTCGTGCC	\$			1231

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGCACGAGC	TGTTGCCGAT	CAGTCCCAT	GACCGCTTGT	ACGACCTTCT	GGGANTTGGG	60
ATACCCAACC	AAGGGGGTAT	CCTTTACTCC	TCCTAGAGT	ACTTCGAAAA	AGCCCTGGAG	120
GAGCTGGCAG	CAGCGTTTCC	GGGTGATGGC	TGGTTAGGTT	CGGCGCGGGA	CAATACGCC	180
GGCAAAAACC	GCACCCAGCT	GAATTTTTTC	CAGGAAGTGG	CGACCTCGA	TGCTCAGCTC	240
ATCAGCTTGA	TCCAGGACCA	GGCCAAACGG	GTCCAGACGA	CCCGCGACAT	CTTGGAGGGC	300
GCCAAGAAAG	GTCTCGAGTT	CGTGGCGCCC	GTGGCTGTGG	ACCTGACCTA	CATCCCGGTC	360
GTGCGGCGAG	CCCTATCGGC	CGCCTTCCAN	GCGCCGTTT	GGCGGCGCGC	GATGGCCGTA	420
GTGGGCGCGG	CGCTTGCCTA	CTTGGTCCGT	AAAACGCTGA	TCAACGCGAC	TCAACTCCTC	480
AAATTCCTTG	CCAAATTGGC	GGATTTGGTC	GCGGCGGCCA	TTGCGGACAT	CATTTCCGAT	540
GTGGCGGACA	TCATCAAGGG	CATCCTCGGA	GAATGTGTGG	AGTTCAATAC	AAACCGGCTC	600
AACGCGCTGA	AAGAGCTTTG	CGACAGCTC	ACGGGGTGGG	TGACCGGACT	GTTCCTCTGA	660
GGTGTGTCGA	ACCTGGAGTC	CTTCTTTGCG	GGCTTCCCGG	GCTTGACCGG	CGCGACCGAG	720
GGCTTGTGCG	AAGTGAATCG	CTTGTTCGGT	GCGGCGGCTC	TGTCCGCTTC	GTCCGGCTTG	780
GCTCAACCGG	ATAGCTGGGC	GAGCTCAGCC	AGCTTCCCGG	CCCTGGCCCG	CATTGGGGGC	840
GGGTCCGGTT	TTGGGGGCTT	GCCGAGCCTG	GCTCAGGTCC	ATGCCGCGTC	AACTCGGCG	900
GCGCTACGGC	CCCGAGCTGA	TGGCCCGGTC	GGCCCGCTCG	CGGAGGAGGT	CGCGCGGCGG	960
TGCGAGCTGG	TCTCGCGGCA	GGTTTCCCAA	GGTATGGGCG	GACCGGTAGG	CATGGGCGGC	1020
ATGCACCCCT	CTTCGGGGGC	GTCSAAAGGG	ACGACGACGA	AGAAGTACTC	CGAAGCGCGG	1080
GGGCGGGCCA	CTGAAGACGC	CGAGCGCGCG	CCAGTGGAAG	CTGACGCGGG	CGTTGGGCAA	1140
AAGGTGCTGG	TACGAAACCT	CTCTAACCG	CATGGCGAGC	CAATCCAT	GCTAGCCAGC	1200
GCCTAACCAAC	GCGCAATGCT	AAACGGGAGG	GACAGGATCA	ATGACGGAAA	ACTTGACCGT	1260
CCAGCGCGAG	CGTCTCGGTC	TACTGGCGTC	GCACCATGAC	AACGCGGCGG	TGATGCTCTC	1320
CTCGGGGCTC	GAAGCTGCGG	CTGGCCTAGG	CGAATCTGTG	GCGATCACTC	ACGGTCCGTA	1380
CTGCTTACAG	TTCAACGACA	CGTTAAATGT	GTACTTGAAT	GCCCACAATG	CCCTGGGCTC	1440
GTCTTGTGAT	ACGGCCGCTG	TGATCTCTCG	CAAAAGTCTT	CGAATTGCGG	CGAAGATATA	1500
TAGCGAGGCC	GACGAAGGCT	GCGCGAAGGC	TATCGACGGG	TTGTTTACCT	GACCACTTTT	1560
GCTGCGGCGA	GTGCGGCGCA	CGACGTAGCG	CAGGTCGTGT	CCCTGTTAGG	CGTGGATGCG	1620
ACCGGCGAGC	ACCAGCACCC	GCTGCGGACC	GATGGGCGAG	GACAGTAGCT	CGCCCGCATG	1680
CCCGGCTGCG	GTGCGGCGCA	CAAACTCGGG	CAGTTCGGCC	TGCGGCGAGC	CGGTGCTTGG	1740
GGAGCCCAAC	GCGGCAACGG	CGGTAACCA	TCCCGACCGG	AGCAGGACCG	AGACCTCATG	1800
TTGCGCGATC	CGGCTGCGGT	CAGCGATGAC	CTGCGCGGCG	CGCGGGGCGA	GTTCGTGCGG	1860
ATCGGGGCGC	GGGTGAGGCA	CAGTGGGCGA	GCTTAACTGA	GCCGCTCGCC	GGGAGCGGGG	1920

TCCTNGTCCA	TCAGATACTG	CGAGCATGCC	AGCAGCCAGC	GCATCCGACC	GCGTCGAGGA	1980
ATTGGTGGCG	CGCCGTGGTG	GCGAGCTGGT	CGAGCTGTCC	CATGCCATCC	ACCTCGTGCC	2040
G						2041

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCACCG	CTATCAACCA	ATACTTTCCTG	CACTCCAAGA	TGCAGGACAA	CTGGGGTPTT	60
ACCGAGCTGG	CGGCGCACAC	CGGCGCGGAG	TCGTTCCGAG	AAATGCGGCA	CGCGGAGGAA	120
ATCACCGATC	GCATCTTGTT	GCTGGATGGT	TTGCGGAAT	ACCAGCGCAT	CGGTTCTGTT	180
CGTATCGGCC	AGACGCTCCG	CGAGCAATTT	GAGGCGGATC	TGGCGATCGA	ATACGACGTC	240
TTGAATCGTC	TCAAGCCAGG	AATCGTCATG	TCCCGGGAGA	AACAGGACAC	CACCGAGCCC	300
GTACTGCTGG	AGAAAATCGT	TGCCGAGCAG	GAGAACACA	TGGACTACTT	GGAAACGCA	360
CTGGAGCTGA	TGGACAAAGT	AGGAGAGGAG	CTTTACTCGG	CGCAGTCCGT	CTCTCGCCCC	420
CCGACCTGAT	GCCCCGCTTA	GGATTCTCCG	ATACCACTCC	GGGCGCCGCT	GACAACTCTT	480
AGCATCGACT	CGAACAGCGA	TGGGAGGCGG	GATATGGCGG	GCCCCACAGC	ACCGACCACT	540
GCCCCACCG	CAATCCGAGC	CGGTGGCCCC	CTGCTCAGTC	CGGTGGGAGC	CAACATTATT	600
TTACCGGCAC	TTGTSTTCGG	GGTGCTGGTC	GCTGCGACCG	GCCAAACCAT	CGTTGTGCCC	660
GCATTGCCGA	CGATCGTCGC	CGAGCTGGGC	AGCACCGTTG	ACCAGTCGTC	GGCGGTCACC	720
AGCTATCTGC	TGGGGGGAAC	ACTSKYGGKK	KTGKKGKSKS	KSEMMMECTC	GGTGAICTGC	780
TGGGCGGCAA	CAGGGTGCTG	CTAGGCTCCG	TGGTGGTCTT	CGTCGTTGGC	TCTGTGCTGT	840
GCGGGTTATC	GCAGACGATG	ACCATGCTGG	CGATCTCTCG	CGCACTGCAG	GCGCTCGGTC	900
CCGCTGCGAT	TTCCGTCACC	GCTACCGCGC	TGCGCGCTGA	GGTGGTCCCA	CTGCGGAGCC	960
GTGGCGCGTA	CCAGGGCGTC	TTANGTGGCG	TGTTGGGTGT	CAACACGGTC	ACCGGTCGCG	1020
TGCTGGGGGG	CTGGCTCACC	GACTATCTGA	GCTGGCGGTC	GCGGTTCCGA	CCACCGAGCC	1080
CATCACCGAC	CCGATCGCGG	TCATCGCGGC	GAACACCGCC	CTCGCGGCGT	TGCGGCGCAG	1140
TCCCTTGGGG	AACGTGGTCC	CACAGCGCCA	GAACGGTCCG	AAATGCGATG	GCGGACCCAC	1200
AC						1202

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCGCGCGGCA	GTGGGCCAGC	AGTINGGCGG	GGGGAGCCCG	TTCGGNGACC	AAGAAATCCG	60
CCTGGGCAAG	CAGCCGGGAC	CGCGNACCGT	GATCAGTTNG	GATCGCCGGG	ACCGCGGCGG	120
ACCAANGCCA	TTCCGCCGNT	GAGGAAGTCG	GAANTNTGCG	CAGTGATGAC	GCCCTGCTGC	180
AACGNTTCCC	GGATTGCCGA	GCGGATCGCC	GCGGAACGGC	GTTGCTCACC	ATCGGCGAGC	240
ACCCCTACNG	ACAGGCCCCG	ATAGCTGAAT	GACGCGCGGT	NACCGCGGTC	CGNTCCACCG	300

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NGAATCGGC CCGGANGCAA AAGATCGGTC GGGGCTCCGC CTGCGCGACG ACAGCCACGT 360
TCACCCGCGC GTTATCGGTG GCGCGGATCG CATACGAGGC GCGGTCAAGG TNGCCGTTCG 420
GGTAGTCACG CACCGACAAG GTGATTTGGT CCATCGGCTN GACGCGGGGG GTGACGCTGG 480
GGGCGATCAM GTGCAC 496

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

TGGATTCCGA TAGCGGTTTC GGGCCCTCGA CCGGCGACCA CCGGCGCAG GCCTCCGAAC 60
GGGGGGGCGG GACGCTGGCA TTGCGCGGGA CCGCAACCAA AGAAGCGCCG GTCCGGGCGG 120
TGGGGCTGAC CCGACTGGCC GTTGATGAGT TCGGCAACCG CCCCCGGATG CCGATGCTGC 180
CGGGGACCTG CGAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGBAGAGGGG 240
GAGGCGACCG CTTACCGCAC GACAGCAAGT AACCGARTTC CGAATCACGT GGACCCGTAC 300
GGGTGAAAG GAGAGATGTT ATGAGGCTTT TGATGCTCA TATCCCAAG TTGGTGGGCT 360
CCCAGTGGGC GTTTGCGGCC AAGGCGGGCC TGATGCGCA CAGATCGGT CAGGCCGAGC 420
AGGCGGCGAT GTGCGCTCAG GCGTTTCACC AGGGGAGTC GTGCGCGCG TTTCAGGCCG 480
CCCATGCCCC GTTTGTGGCG GCGGCGGCGA AAGTCAACAC CTGTGTTGAT GTCGGCCAGG 540
CGAATCTGGG TGAGGCGGUC GGTACCTATG TGGCGCGGGA TGCTGCGGCC GCTCGACCT 600
ATACCGGGT CTGATCGAAC CCTGCTGACC GAGAGGACTT GTGATGTCG AAATCATGTA 660
CAACTACCCC CGCATGTTTG GTACGCGCCG GGATATGGCC CGATATGCG GCACGCTGCA 720
GAGCTTGGGT GCGGAGATCG CCGTGGAGCA GCGCGGTTG CAGATGCTT GGCAGGCGGA 780
TACCGGATC ACGTATCAGG CGTGCGAGGC ACANTGTTAA CCAGGCCANG GAAGATTTCG 840
TGCGGGCCT 849

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1           5           10           15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20           25           30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35           40           45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
50           55           60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65           70           75           80

```

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:110:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	Ala	Ala
1				5				10						15	
Asp	Ala														

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGCACGAGA	ATGTGGCCTG	TGCTTCGATA	GCCACTTGCG	TGTGGTCGCG	CTGCCAGCGG	60
GTCAGCCAGG	TGCGCTGGTC	CAGGCCATCG	GGCCGGGCGA	GGAGCGCGAT	GTTGGCCAGA	120
CCCCGTGTAC	GAGAACCGGA	CTCGACNAAG	TGTCGGGCGT	GACCGCGGCT	CAGTTCGCGG	180
CACACGCCCC	GATCTATCAG	CCCCATCAGG	CCGAGGCGCG	GGCGATTGAC	GAGATGTTCC	240
TCAACACTCT	ACAGATNANC	TCAGGGTCGT	ATGCTGCTAC	CGAGGCGGCT	AACGCGGCGG	300
CGGCCGGCTA	GAGGAGTCAC	TGCGATGGAT	TGTGGGCGGT	TGCGGCGCGA	GCTCAATTCC	360
GTGCGGATGT	ATGCGGCTCC	TGCTTCGGCA	CCAATGGTCC	CTGCGGCGTC	GGCCTGGAAC	420
GGGTTGGCCG	CGGAGCTGAG	TTCGGGCGCC	ACCGGTTATG	AGACGGTGAT	CACTCAGCTC	480
AGCAGTGAGG	GGTGGCTAGG	TCCGGGCTCA	GGCGGATGCG	CCGAGGCGAT	TGCGCGGTAT	540
GTGGGCTGGA	TGAGTGCCGC	TGCGGCGCGA	GCCGAGCAGG	CGGCCACACA	GGCCAGGGCC	600
GGCGCGCGCG	CTTTTGAGGC	GGCGTTTCCG	GCGACGGTGC	CTCCGCGGTT	GATCGCGGCG	660
AACCGGGGCT	CGTTGATGCA	GCTGATCTCG	ACGAAATGCT	TGCGTCAGAA	CAGCTCGGCG	720
ATCGCGCGCG	CCGAAGCTCA	GTACGGCGAG	ATGTGGGCGG	AAGACTCGCG	GGCGATGTAT	780
GCCTACCGCG	GCAATTGCGC	GAGCGGCTCG	GCGGTGCGCG	CGTTTAGCAC	GGCGCGCGAG	840
ATTGCCAACC	CGACCGCTCA	GGGTACCGAG	GGCGCGGCGG	TGGCCACCGC	CGCGCGTACC	900
GGCAGTCTGA	CGCTGACGGA	GATGATCACC	GGGCTACCCA	ACCGGCTGCA	AAGCCTCACC	960
TCACNTCTGT	TGCACTGCTC	TAACGCTCCG	CTGTGTGGGC	TGTGGCAGAT	CTTGTTCGSC	1020
ACGCCCAATT	TCCCCACCTC	AATTTGGGCA	CTGCTGACCG	ACCTGCGAGC	CTACCGGAGC	1080
TTTNTNTATA	ACACCGAGGG	CCTGCCGTAC	TTCAGCATCG	GCATGGGCAA	CAACTTCATT	1140
CAGTCGCGCA	AGACCGTGGG	ATTGATGCGC	TAGGCGGCGC	CGGCTGCGGT	CGCGGCTGCT	1200
GGGGATGCGG	CCAAGGGGCT	GCTTGGACTG	GGCGGGATGC	TGGGTGGCGG	GGCGGTGGCG	1260
GCGGCTCTCG	GCAATGCGGC	TTCGGTGGGC	AAGCTGTGCG	TGCGGCGGCT	GTGGATGGGA	1320
CCGTGCGCGG	GGTCCGCTAC	TCCGCGGCGT	GCTCCGCTAC	CGGTGAGTAC	GCTCAGTGGC	1380
GGCCCGGAGG	CGCGCGCGCG	AAGCCTGTTG	GGCGGCGCTG	CGCTANCTGG	TGCGGCGCGG	1440
GGCGGCGCGG	GTCCACGCTA	CGGATTCGCT	CCGACGCTCA	TGGCTGGGCG	ACCTTCGMC	1500
GGGATAGTGG	CTGCCGCAAC	GTATTAAAGC	GGCGGCGCTG	GCTGGTGTGG	TCCGCTGCGG	1560
GTGGCAATTA	GTGCGCGCGG	AAATCTGCGT	GGGTTATTTT	CGGTGGGATT	TTTTCCCGAA	1620
GGCGGCTTCA	GCACCGGATT	TCTAAGCGGT	CCCGGCACTC	TGCTGCCGAA	TTGCGCACTA	1680
AGTGACGCTC	GGCGGAAACC	GTTGGGTTNT	GAAAGCTTCA	GAAAGGCGCG	CTCCCAAGGG	1740
TTGCGCAAAAC	GG					1752

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Met Asp Phe Gly Ala Leu Pro Pro Gln Val Asn Ser Val Arg Met Tyr
 1          5          10          15
Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
 20          25          30
Gly Leu Ala Ala Gln Leu Ser Ser Ala Ala Thr Gly Tyr Gln Thr Val
 35          40          45
Ile Thr Gln Leu Ser Ser Gln Gly Trp Leu Gly Pro Ala Ser Ala Ala
 50          55          60
Met Ala Gln Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
 65          70          75          80
Ala Gln Ala Gln Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
 85          90          95
Phe Gln Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
100          105          110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
115          120          125
Asn Thr Ser Ala Ile Ala Ala Ala Gln Ala Gln Tyr Gly Gln Met Trp
130          135          140
Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
145          150          155          160
Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
165          170          175
Thr Ala Gln Gly Thr Gln Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
180          185          190
Ala Gln Ser Thr Leu Thr Gln Met Ile Thr Gly Leu Pro Asn Ala Leu
195          200          205
Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
210          215          220
Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
225          230          235          240
Ser Ala Leu Leu Thr Asp Leu Gln Pro Tyr Ala Ser Xaa Xaa Tyr Asn
245          250          255
Thr Gln Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
260          265          270
Gln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
275          280          285
Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
290          295          300
Met Leu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
305          310          315          320
Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
325          330          335
Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala

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	340		345		350
Ala	Pro	Glu	Ala	Ala	Pro
			Gly	Ser	Leu
			Leu	Gly	Gly
			Leu	Pro	Leu
			Kaa		
	355		360		365
Gly	Ala	Gly	Gly	Ala	Gly
			Ala	Gly	Pro
			Arg	Tyr	Gly
			Phe	Kaa	Pro
			Thr		
	370		375		380
Val	Met	Ala	Arg	Pro	Pro
			Phe	Kaa	Gly
			Ile	Val	Ala
			Ala	Ala	Ala
			Thr	Tyr	
	385		390		395
					400

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGCAGGAGCA	CCAGTTGACC	CCGGAAGAAC	CTGACCGCGC	CACCCAGCGC	CGCCCGCATE	60
ACCGGCCCCG	TCCCAAGAAC	CTTTTCGGTA	AACGAGCCAC	TCCAGCGGAG	ATCGGTACCG	120
CCCGAGCGAT	TTGGTGTAA	GACCACCTCG	CCGAAGTAGT	CCTGGACGGG	TGTCTCGCG	180
CCAACCACT	TGTAGACCTG	GCGACGGTCC	TGCTCATACT	CGACGGTCTC	TTCTTCGACG	240
AACACCCGCC	ACATGCTTAG	TTTGCGGATG	GCCCCGATCC	CGCCCGCGCC	GGGATCACCG	300
CGTCGCGCCG	AACTCGATTG	AGCAACGATG	GGCTTGCCCC	AGGTGCCCCA	GTTGCCACCG	360
TCTGTCACGA	GCCGAACAA	GCTTGCGAGC	GGCGCGCTGC	TGGTCTTGGT	GACCTCGAAC	420
GAAATTTCC	GACCGGACAT	GCGCGACTCC	CGAAACGACA	ACTGAAGCTC	GTCC	474

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCCGCGCG	GAAAAAANTA	TTACTGGCAG	GACCGGCAGA	ATGCATGGTG	ATATTCCGGT	60
GATGAGCCCG	CCGAGGAACC	GACTAGTGCG	AGGTCGAACA	CATCGGTTAT	TGGTTGCCGT	120
TTAGGTCTTG	GATCTGCCCG	GACCGCAACG	AGTTGGCAGG	ACCGCTCAGG	CGAGCGCTGT	180
TGACAGAGTC	GGTTCAGTTC	GAACTCGCCA	CCCGTCAGAT	GCGAATGATA	GCCACATCGG	240
CCACACCATC	GACCGCGCTG	AACTCGCCGT	CGTGGGTCAE	GACCGGCACC	CCTTSCGACG	300
TGGCAACGGC	AGCGGCGCTC	ACCGGACGGG	ACCGAGATCG	TGGTGGGTGT	CGCTACTGAG	360
CGTTCGAGCG	TGCGGGGTGC	AATCCCGCAT	CTGCTTCGCT	ATGCCGAGGC	CGCCGCGAGCA	420
GCTCGTCTCG	ACTCAACCAT	CGGCGCGCGT	CGGCTGCGCT	GCGGTGAGCA	GCGCAACGGG	480
TTTGCCGTTG	GCACTGATGG	TGATGTCTTC	GCGCGGCTTC	ACCGCGCGTA	GCAAGCCCGG	540
GGTGTGTTTG	CGCAGTTCCG	GAGACCGGAC	TTGAGCGAGC	ATGCTTCGGG	GATCGGCTTG	600
CGCTGGGCGC	GGTGTACCG	TCATCGGCTT	GGGATATCAC	GTGATCTATC	GGCACGAAGC	660
CGCCGAGTGA	GCGAGGCATA	CGGCTAGCAC	GGGCTGCGCT	GCTTTCACCG	CGCCGAGAGT	720
TACTGTGCGG	GGGTCATCAG	CACCGTATCG	ATCATGTACA	CCGTGCGCTG	GCGGTTGTGA	780
CTCCGCGGCA	TACCAACCGG	GCGTTGTTGA	CCATGAGTGC	TGCGGGGCGC	CTATCACCGT	840

CAGGTGGGCA	CUTTGCAGGT	CTGATGGGTT	CCGTGATATC	TGCTCGGACT	CGCTTGGGCG	900
GCTATCAGGT	GCTAGGTCAG	GATGCTGCTG	AGCAGCTTGG	CGTCACTCTT	GAGTTGATCG	960
ATAGTGGGCG	CCGGCAGCTT	CTGSAATGCG	GGTTTGGTGG	GGGCUAAAAC	GGTGTACTCG	1020
CGGCGGTGGA	GGGTGTGAC	CAGATTACAA	TCCGGGTTCA	GCTTGGCCGA	CAGAGCCGAG	1080
GTGAGGTAC	TGAGCATCGG	GTGTGGA	CCCGCGGTAG	CGACCGGTC	TTGCGCCATT	1140
CCGCGCACCG	ATCCGGGACC	GGTGGGATTT	TGCGCCGCT	ATTGCGGSCA	CCCAGGACCA	1200
ATCAGGTCCG	CTGCGGTGAG	CCATTGCGCG	CGTGTAAAG	GGCGCCGCGG	GGCTGGTCCG	1260
CGGTTTCCGG	CTGGTGTCTT	CGGACACGGG	TTTGTGCTC	GAACAACCGG	CTAGGACCGC	1320
AATCGCGATG	GCTGCGAGGC	TGCTGCTGC	GGCGGTTTG	GCCTGAACGT	TGATCATCGC	1380
TTGATTCCT	TTGCTTCTGC	GCGGCGCTTG	AAGCCCTCC	TGCTGGGTGG	A	1440

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCAGGAGAGT	CTATCTTTG	CACCCAGCGC	CCCTAGGAAA	CCGCTGGGCT	GGTAACTCA	60
GATGCGGGCG	GCCTGCGATT	CGAGAGGTAA	CCGATCGCCC	GGUACAATG	GTTACCCAC	120
CGAGACTGAT	TGCCCGGCG	CCGCTTCGA	CGTGTAAAGG	CGGTTGCTG	CATGCGCGGA	180
ACGGCTGCAC	TCACGGACCT	TCTACGTAGT	ACGTGACGGA	CTTTACGCA	TTATGCTGA	240
GTATCTTGGC	CTCCCAAGGAC	TCCAGAATCT	ACTGTTGCC			279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACCGCCACCG	GCAGCCCGGA	ATCACCGTCS	GTAACCTGCG	AATACAATTT	CTTCATCGAC	60
GACTTGGGGA	ACAGCGAACC	CGAGCCGACC	GCCTGATAGC	CTTCTTCTTC	GATGTTCCAA	120
CCGCGGCGCG	CGTCGAACGA	AACGATACGA	CCCGCGTCTT	GGGGGTGAGA	CGCATGAATG	180
TGGTAGCCCG	CCAGCAACCG	CAGCGCCAGC	AGAGGCTGCA	TGCGGGCGCG	CAGTTTSCCA	240
CGCACCATAA	TGCGCAGCCG	GTTGATTTTG	CCGCGAAGCG	TCAGCGGCGC	ACCTTCGAGC	300
TTCTCGTAGT	GCTCAAGTTC	CACCGGCTAC	AGCCGGGCAA	ACTCAACCGC	GACCGCAGCC	360
GTGCGAGCGA	TGCCGGTAGC	GGTGTAGTCA	TGGTGTATAT	ACACCTTGCG	CACATCAGCG	420
CCAGAAATCA	TGTTGCCCTG	CGTCGAAGCG	CGTTCACCGG	CCATGACAA	ACCGCCGGGG	480
TATTTACCGG	CGACAATGGT	GGTGGCGTGC	GGCAGTTGCG	CATCGCCGCG	TGCGAGTGGC	540
GCACCGCCCG	TGATGCTTGC	CGGCAGCAAC	TCCGCGGCTT	GGCGGGCGCG	GAAGTCAAGT	600
GAAAGAGAGT	AGGTCTACAG	CGGGTGTTC	AGAGAGTGAA	TAAATGACCA	GGCGATCGCG	660
CAACGCGCAG	GTCAGTGTCC	GGCCTTTTGG	ACGTATGCGC	GGACGAAGTC	CTGGGCGTTC	720
TCTTCGAGGA	CGTCGTGAT	TTGCTCGAGC	AGATCGTCCG	TCTCTCGGT	CAGCTTTTCG	780
CGACGCTCCT	GGCCCGCGGC	GTTGCTGCGG	GCGATGTGCT	CATCATCGCC	GGCGCCACCG	840

CCACGGTTCG	TCTGCTCTTG	GGCCATGCGC	GCTTCCTGCT	TGCTCATGGC	CTTTCAAAAG	900
GGCGCGGGTG	CGCGTCACAC	GCCCCCTGTC	TTTCTCTCAC	CTACCGGTCA	ACACCAACGT	960
TTCCCGGGCT	AACGAGGCTT	AGCGAGGCTC	AGCGGTTCAGT	TGCTCTACCA	GCTCCACGGC	1020
ACTGTCCACC	GAATCCAGCA	ACGCACCAAC	ATGCGGCTTA	CTACCCCGCA	ACGGCTCCAG	1080
CGTCGGGATG	CGAACCAGCG	AGTCGCGGCT	AGGTGGAAGA	TCACCGAGTC	CCAGCTAGCC	1140
GCGGCGATAT	CAGCCCCGAA	CGGGGCGAGG	CATTTCGCGG	CGGAAATACG	CGCGGGTGTC	1200
GGTCGGCGGT	TCTCCACCGC	ACTCAGCACC	TGGTGGTTTG	GTGACTAAAC	GCTTTATCGA	1260
GCGGCGGCGG	ACCAGCGGGT	TGTACAGGCG	CTTGTCCAGC	CGGACATCGG	AGTACTGCGG	1320
GTTGACGAGG	TGCAGCGCGG	GCGCCGACCA	GCTCAGGTTT	TCCCGCTGCC	GGAAACCGTC	1380
GAGCAGCGCG	AGTTTGGCGG	GCCAGTCCAG	CAGCTCGCGG	CAATCCATCG	GGTCACGCTC	1440
GAGCTGATCC	AGCAGGTGTG	CCCAGGTTTC				1470

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTCCGATCG	CTCCGGCACC	TATCACCAGG	TACTCGGTTT	CGATGGTTTT	CGCGGGCCCT	60
TGCGTTGGCC	TGGGCCACGG	GTGCTTCATG	GGCCCTCCTG	TGCGKATTCG	AATTGTGAC	120
AACGAAATCG	GGCGATCGGT	GAGCAATCGT	CGCGGATGCA	AGACACGGTT	TGCGTGGCGC	180
GGCGTCAGGT	GGAGTTTAGG	CCAGCGTAAAC	AACGTAGACC	GGCCACTGAC	CAAAACCCCA	240
ACCCACAAAC	CCTGGAAGCA	TGCGGGTCTC	GGCGCTCAGA	TTCGGGGTAG	ATATCGTATA	300
CGGATATCGG	ATGCCGTAGC	CTTATCGAGG	CATGAGACGC	CCGCTAGACC	CACCGGATAT	360
TCCAGATGAG	CTGCGGCGAC	GGCTGGGGCT	CYTGATGCGG	GTGCTGATCG	GGCTTGGGTC	420
CATGATCGGT	GGCGGAATCT	TGCTCGGTGC	CGAATTGGGC	ACGAGCTCGT	GGCGAATTCG	480
GCACGAGATT	CCAAATCCCA	GAAGGTGCTA	CAAGCCGTCA	ATGGCACTTG	ATCGTTGGAT	540
CGATGATGAA	CGCTCTGCTC	ATGCTTGCCG	CCTATCTCAA	CGGTGCTCGA	TTCATGCGAT	600
TAGCTTTGGT	TCTGCATTGC	ACCGGTAGGG	CCTACAGTCT	GGCTGTCTAG	CTTGGCCGAT	660
GTCAACAGTT	TTTTTCATGC	TAAGCAGATC	GTCAGTTTTG	AGTTGCTGAA	GACGGCATGT	720
TCACTTGTTC	TGACTACAT	CGTCTGCGCA	CATTTGCCCT	CCTGCAACTG	CGCTGCGACA	780
ATGCCGCCAC	CGCCGTGTAG	CTCGTGCGCA	ATTGCGCAGG	AGGATCCACC	GGAGATGGCC	840
GACGACTACG	ACGAGGCGTG	GATGCTCAAC	ACCGTGTTCG	ACTATCACAA	CGAGAACGCA	900
AAAGAGAGAG	TCATCCATCT	CGTGCGCGAC	GTGACACAGG	AGAGGGGGCC	CATCGAAGTC	960
GTAACCAAGG	TAGACAAAGA	GGGACATCAG	ACTGCTCTAC	GATGGGGAGC	CACGTTTTCA	1020
TACAAGGAAC	ATCCTAAGTT	TTGATTCGGG	AACATCCTA			1059

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

GCACGAGGCA TTGGCGGGCA TCTGCATAAA CGGTGACCTA TCAGCACAAA ACAGCGGAGA      60
GAACAACATG CCAACAGAAC GTCTCCGGTG GCTGGTAGCC GCAGAGGCTC COTTCGCCCTC    120
GGTGTATTTT GACCACTGCG ACCACTCGTG CCG                                     153

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CCCCCGGGTC GATCAGCGAG CCAGGCAAAA ACTCCGTGGA GCGCGAGTCG ATGATGCTCA      60
CCCCCGGCGAG CATCTGGGGA ACGATCACCT CCAATGCTCT GTCTGGATC GACACACCTT    120
GGGCGCGGTA GACCTCCCTG ACCTCGCGAA CCAGGTGTAT CTGCACCTCG CGGGGGCCCT    180
GCACCGGCAAG CACCTCATGC GGGTCGGCCG AGCCTTCCAT CAGCTGCTGG CCCACCTCGA    240
CGTGTTCGCC ATCGGAGAGC ACCCGTTCGG AACCGTCTTC GTGTTGAAC ACCCGCAGCC    300
GCTGCCGCTT GGAGATCTTG TCGTAGACCA CTTCCTCACC SCCTGCTCA GGAACGATGG    360
TGATCTTGTG GAACCGCTCG CCGTCCT

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GTTCAAGCAAG GGTATCCGAT TGTCCGTTT GCTTCGGTGG GTGCTGAACA CGGCATCGAC      60
ATCGTCTCTG ACAACGAATC CCACTGCTG GCACCGCTCC AGTTCCTCGC CGAGAAGCTG    120
CTCGGCAACA AAGACGGTCC GGCCTGGTC CTTGGTGTCT GACTGACACC GGTACCGCGC    180
CCCGAACGGC AGTATTACTG GTTCGGCGAG CCAACCGACA CCACAGAGTT TATGGGGCAG    240
CAAGCCGAGG ATAAAGCCGC ACGCAGGGTG CCGAGCGGTG CCGCCCGCGC TATCGAACAC    300
GGCATCGAGC TGATGCTGSC CAGCGCGGCA GCCGATCCAA ATCGATCCCT GGTCCGACGG    360
CTCTTCGCTT CGGACGCTTA AGCCGCCCC

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCCCCGCTCG	GAATGATCCC	CCTCTCGTCC	CCCGCCCAT	TGATGCTGTT	GATGAGCTGT	60
TTGGAGAGGC	CCGTTGSCS	TACCGGTGAG	CCGGAATATC	TGTTGGAAAC	GTACCCGGAT	120
GTNCACATGA	ANTNONTGON	CCCGTNGCCG	CTNTTGCNTG	NGNAAACAC	GTGTTGTNTA	180
AGCCTTONTG	GNCTCGNAAG	NGCCGTNGAC	GCCTGTGTCC	CCGAAGATAA	TGAGCACCTG	240
ACGTTTGGCU	GGATCGCCCT	TATCCCAAGG	AATTCGAGG	TGGTCCCCGG	AGATGCCGAA	300
GCCTTCCAGS	GTCTGTGTCG	GGCTGTCCGG	TCCGTCACCC	CACTCGCCGA	GGATGTGCGN	360
AGCCCCGGCG	AGCGTGGCAC	CAGGATCCGG	CGCCGCCGCC	GGAGCAGGGT	CGGNNCTGNN	420
NCTGNTTCC	TNNGGCCNAA	TTNNACTCGN	NCAACAANCT	TGNNNCCGAC	TCNNACCGNN	480

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCACGAGGCT	ACCGSCCGCT	CCCCCGCAT	CCCCTGGATG	CACGCGTAGC	CACCCGTNCA	60
TNCAGCGGGT	CAGCUGCCGC	GTCCGGGCTT	AACGCTATAG	CAGTGCUAAA	CAACCCGSCG	120
CCGCAATTA	CTTTGATGTT	GAACCGATGA	CCATNGCCTN	CGNGTNCAT	CTGNTCTCTT	180
NGCGCGCCNC	TATTTNNGCC	ATANATTTGG	TTNMANNCGN	AACGCTAGAC	GTATCGAGTT	240
CCFTTTCGAC	CACCGGCTCA	ATTGTTCAGCA	TCTATGCGGG	AACATGAGCC	CGCGCCGACC	300
GGCGCGTTTC	CAATGCTTGA	CUTCACAACG	GTCTACAAG	CCAGCGCAAT	GTCCCGCGTA	360
GGGACGCGGC	GGCTGGGATC	GGTGGGGTGA	GGCGCCGGCT	TCTCAAGCG	AGGGGAGCCC	420
CGGACTCTT	ACCGSCCGAA	GGCGCGGGT	GTCACTGATC	TAGGCTGAGC	GCCAGTGGTT	480
GNTRAGCCAA	CAAGGATGAC	NACAAATAAN	CCGAGGANAG	ACANGNGACG	GNCCGANANG	540
CTNANCCGGN	NTTGNNCNAA	NNNNACNCAC	TTNTACCGNN	CTTATGNN		587

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCAATGAG	CAGAGCGTTC	ATCATCGATC	CAACGATCAG	TGCCATTGAC	GGCTTGTACG	60
ACCTTCTGCG	GATTGGAATA	CCCAACCAAG	GGGGTATCCT	TIACTCCTCA	CTAGAGTACT	120
TCGAAAAGGC	CCTGGAGGAG	CTGGCAGCAG	CGTTTCCGCG	TGATGGCTGG	TTAGGTTCCG	180
CCGCGACAA	ATACGCGGCG	AAAAACCGCA	ACCACCTGAA	TTTTTTCCAG	GAAGTGGCAG	240
ACCTCGATCG	TCAGCTCATC	AGCTTGATCC	ACGACCGAGC	CAACCGCGTC	CAGACGACCC	300
CGGACTTCCT	GGAGGGCGCC	AAGAAAGGTC	TGAGGTTCCG	CGGCGCGTGG	GCTGTGAGCC	360
TGACCTACAT	CCCGGTCGTC	GGGCACGCCC	TATCGGCCGC	CTTCCAGGCG	CCCTTTTGGG	420
CGGGCCGCGAT	GGCGGTAGTG	GGCGGCGCGC	TTCCTTACTT	GTCGCTGAAA	ACGCTGATCA	480
ACGCGAUTC	ACTCCTCAAA	TTGCTTGCCA	AATGGCGGGA	GTTGGTCCCG	GGCGCCATTG	540
CGGACATCAT	TTGGGATGTC	CGGACATCA	TCAAGGGCAC	CCTGGGAGAA	GTGTGGGAGT	600

```

TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCAGG GCGTGGGTGA 660
CGGCACTGTT CTCTCGAGGG TGSTCGAACC TGGACTCCTT CTTTGGGGGC GTCCCCGGCT 720
TGACCGGGGC GACCAAGGGC TTGTGCAAG TGAATGGCTT GTTCGGTGGC GCGGGTCTGT 780
CGGCATGCTC GGGTTTGGCT CACGGGGATA GCTTGGCGAG CTCAGCCAGC TTGCCCCCCC 840
TGGCCCGCAT TGGGGCGGGG TCGGTTTTTG GGGCTTGGC GAGCCTGGCT CAGCTCCATG 900
CGGCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCGGTTCGGC GCGGCTGCCC 960
AGCAGGTGGG CCGGCAGTGG CAGCTGGTCT CCGCCAGGG TTCCCAAGT ATGGGCGGAC 1020
CGTAGGCAT GGGCGGCATG CACCCCTCTT CCGGGGCGTC GAAGGGGAGC ACGACGAAGA 1080
AATACTCGGA AGGCGGGGGC GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG 1140
ACGCGGGCGG TGGGCAAAA STGCTGGTAC GAAACGTCT CTACCGGCAT GCGGAGCCAA 1200

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1           5           10           15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20           25           30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35           40           45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50           55           60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65           70           75           80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85           90           95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100          105          110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115          120          125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130          135          140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145          150          155          160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165          170          175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180          185          190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195          200          205
Gln Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210          215          220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225          230          235          240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245          250          255

```

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Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
      260              265              270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
      275              280              285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
      290              295              300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
      305              310              315              320
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
      325              330              335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
      340              345              350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
      355              360              365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
      370              375              380
Lys Val Leu Val Arg Asn Val Val
      385              390

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

ACGTTTACCC ATCCCGTCGG TGCAGAGCAA CGCCAGACAA CACAAAGTAG TCTAATTCCG      60
TTATAAAGCA GACATTTCCG TGCTTATGTA GAAGATGTGG ACCGATCAGA TGAAGCGATC      120
CGCTCAGGT GGTATCCGAT GTCCTTTGTG ACCATCCAGC CGGTGGTCTT GGCAGCCGCG      180
ACGCGGGACT TCCCGACGAT CGGTACCGCC GTGAGTGTCT GGAACACAGC CCTCTGTGCC      240
CGACCGACGG GGGTGTIACC CCTGCTGCC AATGACGTGT CGGTCTGAC GCGCGCCCGG      300
TTCACCGCGC ACACCAAGCA CTACCGAGTG GTGASTAAGC CGGCCGCGCT GGTCCATGGC      360
ATGTTCTGTG CCTCCCGG GGCACCGCC GATGCGTATG CGACACCGA GGTCTCAAT      420
GTGGTCGCCA CCGTTAAG

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

GAGGTTGCTG GCAATGGATT TCGCGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA      60
TTCCGGTCCG GGGCCGGAGT CGAGCTAGC CGCCCGCGCC GCTGGGACG CTCTGCCCCC      120
GGAGTTGACT TCCGCCCGCG TCTCGTATGG ATCGGTGCTG TCGACCTGA TCCTTGAGCC      180

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GTGGATGGGG CCGGCGGGGG CCGCGATGGC GGGGGGGGCA ACGCCGTATG TGGGGTGGCT 340
GGCCCCCAGG GCGGCGCTGG CGAAGGAGAC GGCCACACAG GCGAGGGCAG CCGGCGAAGC 300
GTTTGGGAGC GCGTTCGCGA TGACGGTGGC ACCATCCCTC GTGCGGGCCA ACCGCGAGCC 360
GTTGATGTTC CTGGTCGCGG CGAACATTCT GGGGCAAAAC AGTGGCGCGA TCGCGGCTAC 420
CCAGGCGGAG TATGCGGAAA TGTGGGGCCA AGACGCTGCC GTGATGTACA GCTATGAGGG 480
GGCATCTGCG GCGGCGTTCG CTTTGGCGCC GTTCACTCCA CCGGTGCAAG GCACCGGCCC 540
GGCGGGGGCC GCGGCGGCGA CCGCGGCGAC CCAAGCGGCG GGTGCGGGCG CCGTTGCGGA 600
TGCACAGGCG ACACTGGGCU AGCTGCCGCC GGGGATCCTG AGCGACATTC TGTCCGCTT 660
GGCGGCGAAC GCTGATCGGC TGACATCGGG ACTGTTGGGG ATCGCGTCCA CCTCAACCC 720
GCAAGTCGGA TCGGCTGAGC CGATAGTGAT CCCCACCCCG ATAGGGGAAT TGGACGTGAT 780
CGCGCTCTAC ATTGCATCCA TCGCGACCGG CAGCATTGCG CTCGCGATCA CGAACACGGC 840
CAGACCCCTG CACATCGGCC TATACGGGAA CCGCGGCGGG CTGGGAGCCA CGCAGGGCCA 900
TCCACTGAGT TCGCGGACCG ACGAGCGGGA GCGCGACTCG GCGCCCTTCS GCGGCGCGGC 960
GCGGCTGTCC GCGGCGTTCG GCGCGGCGAC ATTAGTCGGA GCGTGTGCGG TGCGCGACAG 1020
CTGGAGCAGG GCGGCGCGCG AGATCCAGCT CCGCGTTCAG GCAACACCCA CCTTCAGCTC 1080
CAGCGCCGCG GCGGAGCGGA CCGCCCTAAA CCGGATGCGG GCAGGCTGCG TCAGCGGAT 1140
GCGTTTGGCG AGCGTGGCGG CACGCGGCAC GACGCGCGGT GCGGCGACCC GTAGCGGCAC 1200
CAGCACTGAC GCGGAGAGCG ACGGCGGCAA ACCCGCGTA GTTGTGATTA GAGGCGAGCC 1260
GCGGCGCGGA AACCGCGCGC GGTAAAAGTC CCGCAACCGT TCGTGGCGCG GCGGAAAATG 1320
CCTGGTGAAG GTGGTATCC GACGCGCGGT TCACACCGCT TGTAGTAGCG TACGCGTATG 1380
GACGAGCGTG TGTGATTCT CCGCGGCTAT CAGAGCGATT TTGCTCGCAA CCTCAGCAAA 1440
G 1441

```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

Met Ser Phe Val Thr Ile Gln Pro Val Val Leu Ala Ala Ala Thr Gly
 1           5           10           15
Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
 20           25           30
Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asn Asp Val Ser
 35           40           45
Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
 50           55           60
Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
 65           70           75           80
Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val
 85           90           95
Ala Thr Gly

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
1				9				10						19	
Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp
		20						25					30		
Gly	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val
	35						40					45			
Val	Ser	Thr	Leu	Ile	Val	Gln	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala
	50					55				60					
Met	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala
	65				70					75					80
Ala	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala
			85					90						95	
Phe	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala
	100							105					110		
Asn	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln
	115						120					125			
Asn	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp
	130					135					140				
Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala
	145				150					155					160
Ala	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro
			165					170						175	
Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly
	180							185					190		
Ala	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile
	195						200					205			
Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr
	210					215					220				
Ser	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser
	225				230					235					240
Ala	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile
			245					250						255	
Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile
	260							265					270		
Thr	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly
	275					280						285			
Gly	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu
	290					295					300				
Pro	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala
	305				310					315					320
Gly	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser
			325					330						335	
Trp	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro
	340							345					350		
Thr	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met
	355					360						365			
Pro	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg
	370					375						380			

Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1 5 10 15
 Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
 20 25 30
 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
 50 55 60
 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu

Gln Xaa Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
85 90 95

Ala Ala Gly

Claims

1. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NO:1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, or a complement thereof under moderately stringent conditions.
2. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 16-33, 109, 126, 138, 141, 142 and variants thereof.
3. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.
4. An expression vector comprising a DNA molecule according to claim 3.
5. A host cell transformed with an expression vector according to claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
7. A pharmaceutical composition comprising at least one polypeptide according to any one of claims 1 and 2 and a physiologically acceptable carrier.

8. A pharmaceutical composition comprising at least one DNA molecule according to claim 3 and a physiologically acceptable carrier.

9. A pharmaceutical composition comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128, and a physiologically acceptable carrier.

10. A vaccine comprising at least one polypeptides according to any one of claims 1 and 2 and a non-specific immune response enhancer.

11. A vaccine comprising:
at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
a non-specific immune response enhancer.

12. The vaccine of claims 10-11 wherein the non-specific immune response enhancer is an adjuvant.

13. A vaccine comprising at least one DNA molecules according to claim 3 and a non-specific immune response enhancer.

14. A vaccine comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128; and a non-specific immune response enhancer.

15. The vaccine of claims 13 or 14 wherein the non-specific immune response enhancer is an adjuvant.

16. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 7-9.

17. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 10-13.

18. A fusion protein comprising at least two polypeptides according to any one of claims 1 and 2.

19. A fusion protein comprising a polypeptide according to any one of claims 1 and 2 and a known *M. tuberculosis* antigen.

20. A pharmaceutical composition comprising a fusion protein according to any one of claims 18 and 19, and a physiologically acceptable carrier.

21. A vaccine comprising a fusion protein according to any one of claims 18 and 19, and a non-specific immune response enhancer.

22. The vaccine of claim 21 wherein the non-specific immune response enhancer is an adjuvant.

23. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 20.

24. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 21 and 22.

25. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with at least one polypeptide according to any one of claims 1 and 2; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

26. A method for detecting tuberculosis in a patient, comprising:
- (a) contacting dermal cells of a patient with at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO:2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO:2-10, 102, 128; and
 - (b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.
27. The method of any one of claims 25 and 26 wherein the immune response is induration.
28. A diagnostic kit comprising:
- (a) a polypeptide according to any one of claims 1 and 2; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.
29. A diagnostic kit comprising:
- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

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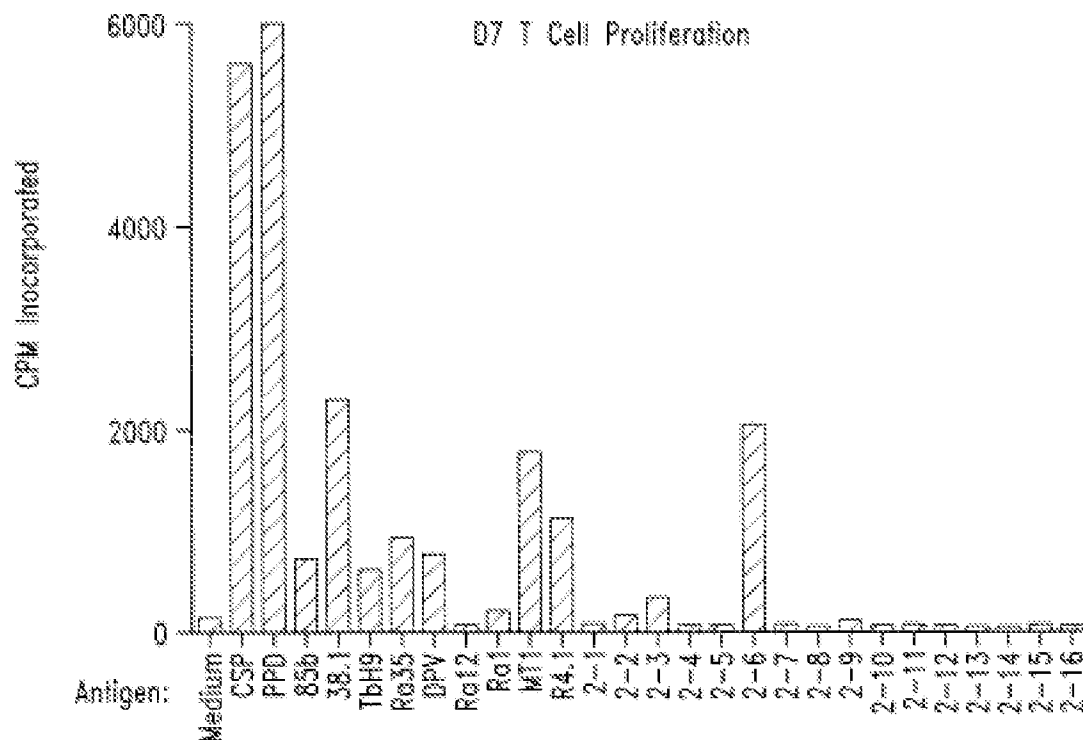


Fig. 1A

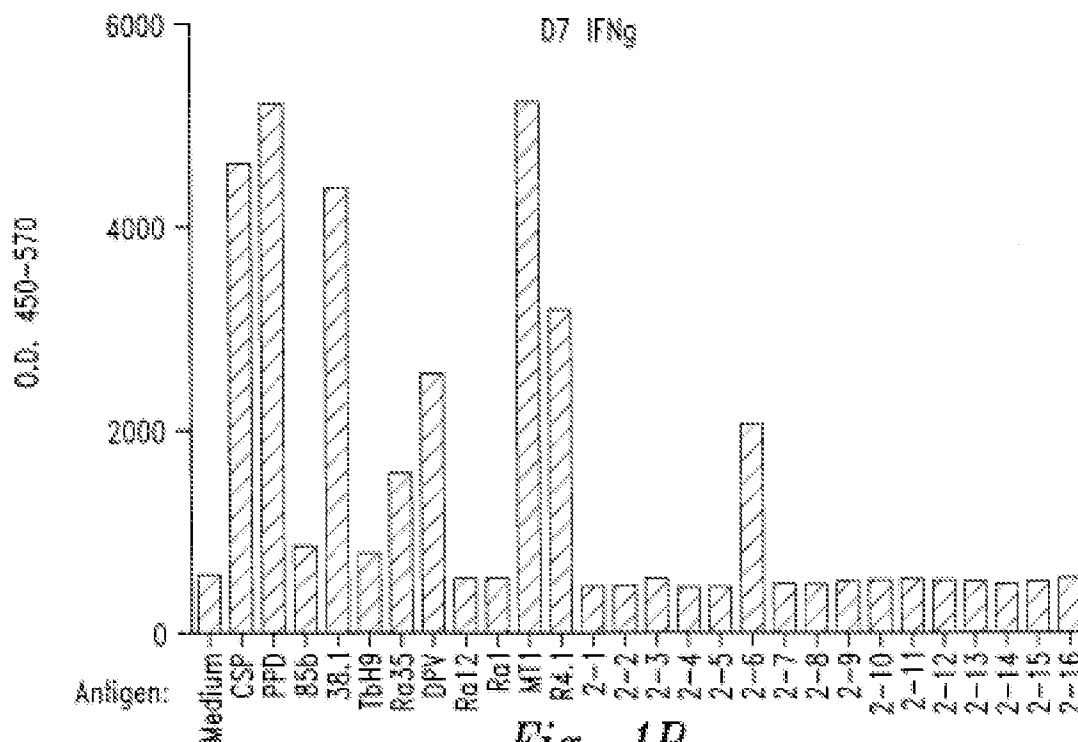


Fig. 1B

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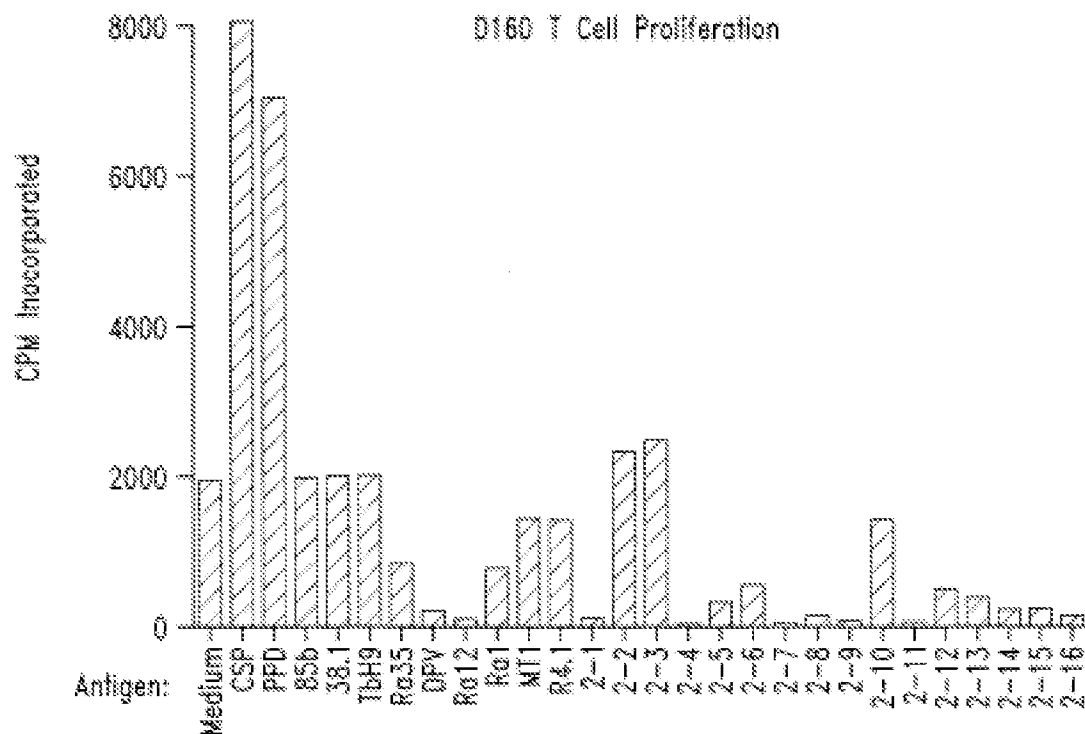


Fig. 2A

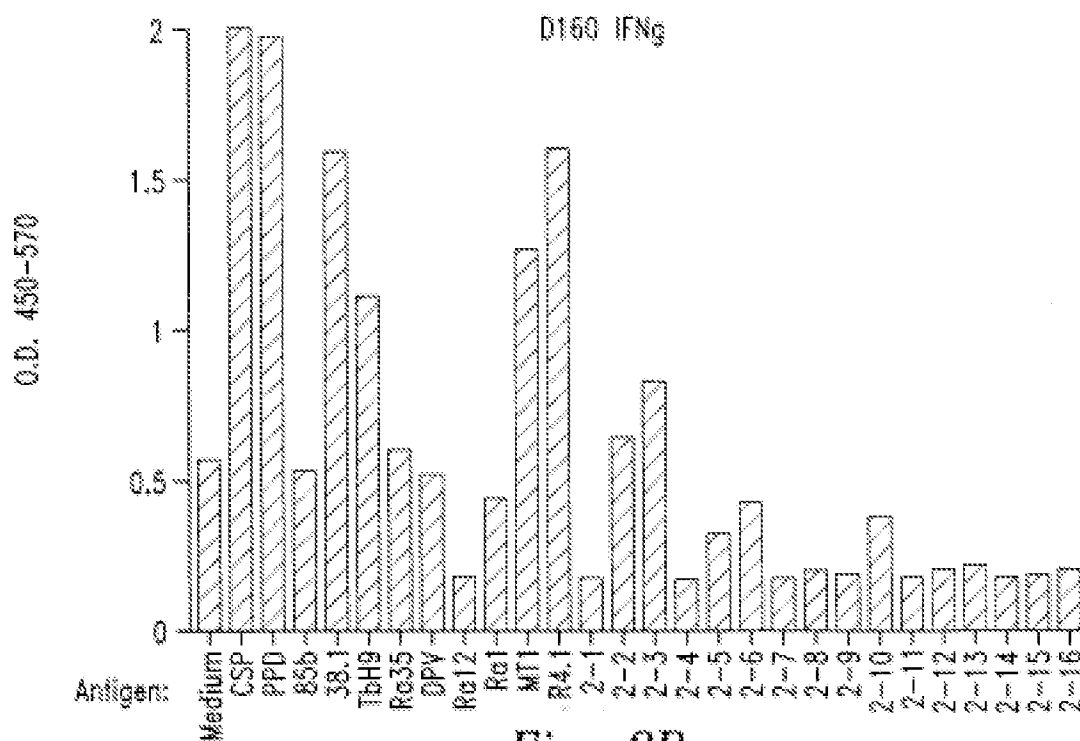


Fig. 2B